

# SEQUENCE LISTING

<110> Godfrey, Wayne  
 Buck, David  
 Engleman, Edgar G.

<120> Receptor on the Surface of Activated T-Cells: ACT-4

<130> 16524.015

<150> US 09/852,845

<151> 2001-05-11

<150> US 08/472,940

<151> 1995-06-06

<150> US 08/147,784

<151> 1993-11-03

<160> 2

<210> 1

<211> 1057

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (15)..(845)

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<223> ACT-4-h-1 cDNA

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Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro	
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tgt gcg gct ctg ctc ctc ctg ggc ctg ggg ctg agc acc gtg acg ggg	98
Cys Ala Ala Leu Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly	
15 20 25	
ctc cac tgt gtc ggg gac acc tac ccc agc aac gac cgg tgc tgc cac	146
Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His	
30 35 40	
gag tgc agg cca ggc aac ggg atg gtg agc cgc tgc agc cgc tcc cag	194
Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln	
45 50 55 60	
aac acg gtg tgc cgt ccg tgc ggg ccg ggc ttc tac aac gac gtg gtc	242
Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val	
65 70 75	

agc tcc aag ccg tgc aag ccc tgc acg tgg tgt aac ctc aga agt ggg 290  
 Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly  
 80 85 90

agt gag cgg aag cag ctg tgc acg gcc aca cag gac aca gtc tgc cgc 338  
 Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg  
 95 100 105

tgc cgg gcg ggc acc cag ccc ctg gac agc tac aag cct gga gtt gac 386  
 Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp  
 110 115 120

tgt gcc ccc tgc cct cca ggg cac ttc ttc cca ggc gac aac cag gcc 434  
 Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala  
 125 130 135 140

tgc aag ccc tgg acc aac tgc acc ttg gct ggg aag cac acc ctg cag 482  
 Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln  
 145 150 155

ccg gcc agc aat agc tcg gac gca atc tgt gag gac agg gac ccc cca 530  
 Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro  
 160 165 170

gcc acg cag ccc cag gag acc cag ggc ccc ccg gcc agg ccc atc act 578  
 Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr  
 175 180 185

gtc cag ccc act gaa gcc tgg ccc aga acc tca cag gga ccc tcc acc 626  
 Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr  
 190 195 200

cgg ccc gtg gag gtc ccc ggg ggc cgt gcg gtt gcc gcc atc ctg ggc 674  
 Arg Pro Val Glu Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly  
 205 210 215 220

ctg ggc ctg gtg ctg ggg ctg ctg ggc ccc ctg gcc atc ctg ctg gcc 722  
 Leu Gly Leu Val Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala  
 225 230 235

ctg tac ctg ctc cgg agg gac cag agg ctg ccc ccc gat gcc cac aag 770  
 Leu Tyr Leu Leu Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys  
 240 245 250

ccc cct ggg gga ggc agt ttc cgg acc ccc atc caa gag gag cag gcc 818  
 Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala  
 255 260 265

gac gcc cac tcc acc ctg gcc aag atc tgacctgggc ccaccaaggt 865  
 Asp Ala His Ser Thr Leu Ala Lys Ile  
 270 275

ggacgctggg ccccgccagg ctggagcccg gagggctctgc tgggcgagca gggcaggtgc 925

aggccgcttg ccccgccacg ctctctgggcc aactctgcac cgttctaggt gccgatggct 985

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 aaaccttggc ag 1057

<210> 2  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> deduced amino acid sequence of ACT-4-h-1

<400> 2

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Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	Thr	Gly	Leu	His	Cys	Val	20	25	30	
Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His	Glu	Cys	Arg	Pro	35	40	45	
Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser	Gln	Asn	Thr	Val	Cys	50	55	60	
Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	Val	Val	Ser	Ser	Lys	Pro	65	70	75	80
Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	Ser	Gly	Ser	Glu	Arg	Lys	85	90	95	
Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp	Thr	Val	Cys	Arg	Cys	Arg	Ala	Gly	100	105	110	
Thr	Gln	Pro	Leu	Asp	Ser	Tyr	Lys	Pro	Gly	Val	Asp	Cys	Ala	Pro	Cys	115	120	125	
Pro	Pro	Gly	His	Phe	Ser	Pro	Gly	Asp	Asn	Gln	Ala	Cys	Lys	Pro	Trp	130	135	140	
Thr	Asn	Cys	Thr	Leu	Ala	Gly	Lys	His	Thr	Leu	Gln	Pro	Ala	Ser	Asn	145	150	155	160
Ser	Ser	Asp	Ala	Ile	Cys	Glu	Asp	Arg	Asp	Pro	Pro	Ala	Thr	Gln	Pro	165	170	175	
Gln	Glu	Thr	Gln	Gly	Pro	Pro	Ala	Arg	Pro	Ile	Thr	Val	Gln	Pro	Thr	180	185	190	
Glu	Ala	Trp	Pro	Arg	Thr	Ser	Gln	Gly	Pro	Ser	Thr	Arg	Pro	Val	Glu	195	200	205	

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val  
 210 215 220  
 Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu  
 225 230 235 240  
 Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly  
 245 250 255  
 Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser  
 260 265 270  
 Thr Leu Ala Lys Ile  
 275